

MMU72677_1	-----	
219_HUMAN	MR-LAG-PLRIIVLVLVSVGVWTIVSILLGGPGSG--FPRIQQLFTSPES	46
D87120_1_1	MR-VAG-AAKLVVAVAVFLLTFYVISQVFEIKMDA--SLGNLFARSALDT	46
z219a.pep	MRPLAGGLLKVVVFVVFASLCAWYSGYLLAELIPDAPLSSAAYSIRSIGER	50
MMU72677_1	-----	
219_HUMAN	SVTAAPRARKYKCGLPQPCPEEHLAFRVVSAGANVIGPKICLEDKMLSS	96
D87120_1_1	-AARSTKPPRYKCGISKACPEKFHAFKMASGAANVVGPKICLEDNVLMMSG	95
z219a.pep	PVLKAPVPKRQKCDHWTPCPSDTYAYRLLSGGGRSKYAKICFEDNLLMGE	100
MMU72677_1	-----	
219_HUMAN	TGQVMKKDSFDMSGD-PQLLNFLTEIPDSTL	32
D87120_1_1	VKDNVGRGLNIALVNGVSGELIEARAFDMWAGD-VNDLLK FIRPLHEGT	145
z219a.pep	VKNNVGRGINVALANGKTGEVLDKYFDMWGGD-VAPFIEFLKAIQDGTI	144
	QLGNVARGINIAIVNYVTGNVTATRCFDMYEGDNSGPMTKFIQSAAPKSL	150
MMU72677_1	-----	
219_HUMAN	VLVASYDDPGTKMNDKIKTLFSNLGSSYAKQLGFRDSWFVGAKDLKSks	82
D87120_1_1	VVFVASYDDPATKMNEETRKLSELGSRNAAKEAFRDSSWFVGAKGVQNks	195
z219a.pep	VLMGTYDDGATKLNDEARRLIADLGSTSITNLGFRDNWFCCGGKGIKTKS	194
	LFMVTYDDGSTRLNNDAKNAIEALGSKEIRNMKFRSSWFIAAKGLELPS	200
MMU72677_1	-----	
219_HUMAN	PYEQFLKNNPET--NKYDGWPELLELEGCVPRKVM--	115
D87120_1_1	PFEQHVKN SKHS--NKYEGCPEALEMEGCIPRSTAS	230
z219a.pep	PFEQHIKN NKDT--NKYEGWPEV VEMEGCIPQKQD--	227
	EIQREKINHSDAKNNRYS GWP AEIQIEGCIPKERS--	235

FIGURE